A stochastic, functional-structural model for cotton plants

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Introduction

Cotton is one of the most important cash crops in the world and a few specific models have been built to simulate and predict cotton plants growth and development, such as L-OZCOT (Hanan and Hearn, 2003). The functional-structural GREENLAB model aims at simulating topological and morphological growth processes at organ scale for general plants (Yan *et al.*, 2004). It has been used to investigate the effects of branch pruning on the source-sink balance of cotton plants, where the deterministic development of plant architectures was considered (Li *et al*., 2009).

However, when grown in the field, cotton has a complex architecture resulting from an intricate pattern of development, which strongly influences its ability to capture resources (Hanan and Hearn, 2003). Therefore, it is important to build a model that would account for the large range of potential plant architectures. Several sources of architectural variability can be identified, such as uncertainties of branches and flowers. Dealing with such variability implies the need of a stochastic version of the GREENLAB model, named GL2 (Kang *et al*., 2008). The calibration procedure, as presented in Wang *et al.* (2009) for young pine trees, requires data not only on an individual plant but on a population of plants. In this study, we will use this model to study the structure development and biomass production of cotton plants and visualize cotton architectures.

Materials and methods

Field experiment

The field experiments were conducted at Quzhou experiment station (36°52' N, 115°1' E) in North China Plain, from 17 May to 15 August in 2007. The cotton cultivar was DP99B (*Gossypium hirsutum* L.). Seeds were sown at a spacing of 2 × 2 m. No mineral or water limitations.

Every week, 60 cotton plants were randomly chosen to count the number of phytomers on the main stem and each branch, respectively. At the same time, three plants were destructively measured to get the fresh weight and area of individual leaf blades, as well as the fresh weight, length and diameter of all internodes and petioles. Root was not taken into account.

Brief description of GREENLAB model

Detailed descriptions of the model were presented in some previous studies (Yan *et al*., 2004; Wang *et al*., 2009) and we just recall its main principles. In the model, the plant architecture is described hierarchically according to their physiological age (PA). The time step, called growth cycle (GC), is the time elapsed between emergences of two successive phytomers expressed in thermal time.

GL2 is a stochastic functional-structural model, where the plant topology development depends on probabilities related to bud functioning (e.g., branching probabilities, etc.). For cotton, we consider that each vegetative branch appears with a probability *p*. As a result, the numbers of organs depend on "*p*". It is possible to calculate theoretically the mean and variances of numbers for organs of each physiological age, even for complicated tree structures (see Kang *et al.*, 2008).

Based on these rules, it is possible to compute the average number of organs in the stochastic plants at each growth cycle, which will be used to compute plant biomass production and allocation among organs.

The equation of biomass production is based on the classical Beer-Lambert's law, adapted for the case of individual plant using a "local LAI" (Yan *et al*., 2004). When the plant is of *i*-GC old, the biomass (*q*) of an organ (*o*) with its age *k* GC is the result of biomass accumulation in past cycles, depending on its ability of acquiring biomass (sink), as follows:

$$q_o(i,k) = \frac{Q(i)\,D_o(k)}{D_t(i)} + q_o(i-1,k-1) \text{ , where } Q(i) = \frac{E(i)\,S_p}{R}\left(1-\exp\left(-\frac{S_b(i)}{S_p}\right)\right) \qquad (1)$$

$Q(i)$ is biomass production at GC i, $D_t(i)$ is the plant demand at GC i, calculated as the sum of organ demands $D_o(i)$ of the plant. $E(i)$ is the average potential of biomass production during GC(i), which can depend on environmental factors. In this study, it was considered as a constant value. $S_b(i)$ is the functional blade area of all the leaves in the whole plant; R is an empirical resistance parameter of the plant; S_p is the ground projection area of the leaves, which takes into account their inclination.
In this study, we use GreenScilab toolbox (http://www.scilab.org) and the Digiplante software (ECP, Cournède *et al*., 2006) to estimate model parameters and simulate cotton growth and development.

Results

Descriptions on cotton structure. The cotton plants grown in low density have a more complicated topological structure than those grown in classical agronomical densities (Fig.1a). They grow larger and have more branches. A developmental pattern can be exhibited (Fig. 1b): along the stem, two main zones can be identified, according to their axillary production: a stem zone (PA 1) with vegetative branches (PA 3), and a stem zone (PA 2) with fruit branches (PA 4) only. Between them there is a small negligible zone with mixed vegetative and fruit branches. Vegetative branches of PA 3 can bear some small fruit branches (PA5).

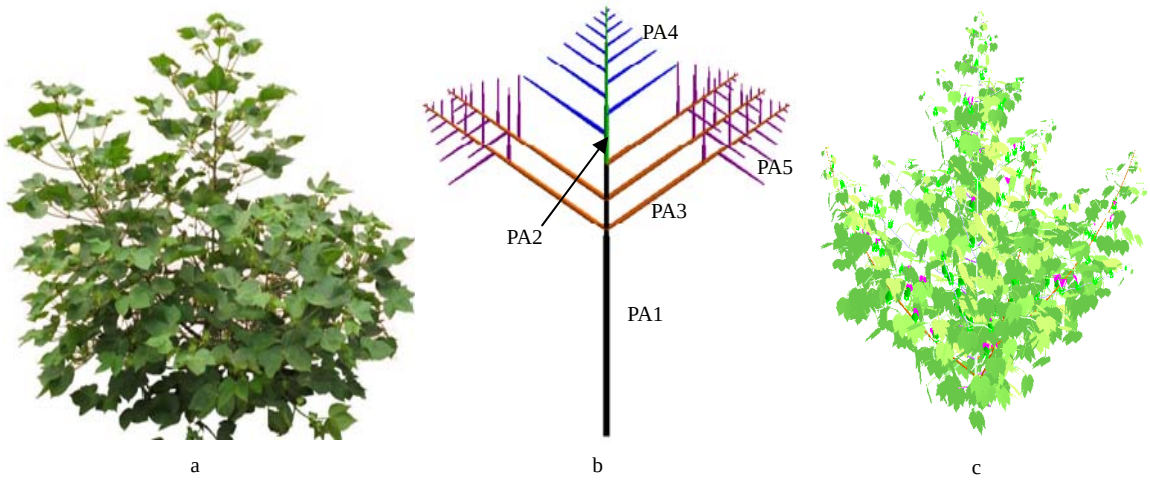

Fig. 1. Topology of cotton. Fig. 1a is a real cotton plant. Fig. 1b shows the schematic diagram of the average cotton, which we used to arrange data in the model. PA1 denotes the main stem zone where the vegetative branches (PA3) appear. PA2 denotes the main stem zone where the fruit branches (PA4) appear and PA5 branches are the fruit branches present on PA3. Fig. 1c represents the simulated cotton based on parameters calibrated from the real data.

The average number of vegetative branches of the 60 plants is 5.2. The branches mostly appeared at position 5, 6, 7, 8, 9 along the main stem, although it can be 3-13 among plants. In real cotton plant, there is one PA3 branch at each node, but the vegetative branches do not appear immediately after the appearance of their subtending internodes, but can wait several cycles before emergence.

So it is observed that the delay of vegetative branches (PA 3) decrease with the branching position, which means that they are nearly synchronous. Therefore, to simplify the structure of cotton, we assumed a virtual cotton plant where the vegetative branches could only appear, without delay, on position 9, 10 and 11 (Fig. 1b). The number of branches at each of these positions is calibrated in order to get the correct number of emergent branches at each time.

It was found to follow a binomial law of parameters (7, 1.74). The position where the branch (PA3) appeared was always 12. The phyllochron of fruit branches (PA4 and PA5) were found bigger than that of the main stem.
According to data, a growth ratio of 0.5 was introduced for these branches, and a phytomer of PA4 or PA 5 can appear every other cycle. Based on these assumptions, the model could reproduce the number of phytomers of each PA at the different measurement stages (Fig. 2a).

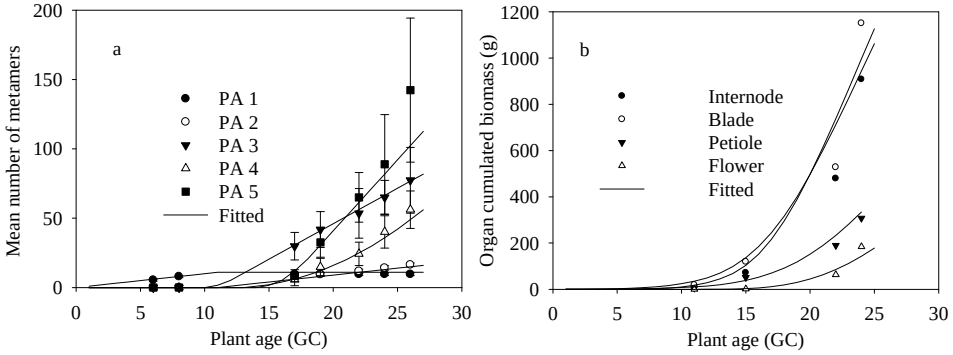

Fig. 2 Fitting GL2 to cotton structures and biomass production. In Fig. 2a, lines are fitted phytomer production with respect to time and dots are means of measured data (n = 60). PA1, PA2, PA3, PA4 and PA5 are specified as in Fig. 1. Fig. 2b shows the fitted and measured total biomass for the cotton plant.

Physiological process. Organ dimensions (e.g. length of internodes, surface of leaves) were derived from their mass by allometric relationships that were estimated from the data for each PA-based class (data not shown). Then, the functional part of GREENLAB was fitted to data from four growth stages (Fig. 2b), to get the hidden parameters.

4. Discussion

Cottons growing in low density have complicated architectures with inherent variability of types, number, positions, and emergence delays of branches, so it is difficult to describe the cotton structure accurately and to build a cotton model at organ level. Based on some simplifications that we consider as relevant, the GL2 stochastic FSPM simulates plants for which the numbers and the mass of phytomers of each PA present in the plant at each GC are consistent with the observations. That model can now be used to simulate individual-based stands with varied structures and functions among cottons. Further works can be considered based on these results. First, the fitting procedure and results (especially the results for PA 5 phytomers, see Fig. 2) could be improved by refining the topological simplification, for instance by taking into account the variability of phytomer production rate. Another research direction is to take into account external factors, such as different densities, to build a more predictive and realistic FSPM-based stand growth model.

References

Cournède PH, Kang MZ, Mathieu A, Barczi JF, Yan HP, Hu BG, de Reffye P. 2006. Structural Factorization of Plants to Compute Their Functional and Architectural Growth. SIMULATION, 82: 427-438.

Hanan JS, Hearn AB. 2003. Linking physiological and architectural models of cotton. Agricultural Systems, 75: 47-77.

Kang MZ, Cournède PH, de Reffye P, Auclair D, Hu BG. 2008. Analytical study of a stochastic plant growth model: Application to the GreenLab model. Mathematics and Computers in Simulation, 78: 57-75.

Li D, LETORT V, Guo Y, de Reffye P, Zhan ZG. 2009. Modeling branching effects on source-sink relationships of the cotton plant. In: Guo Y, Jaeger M eds. Proceedings of Plant Growth Modeling and Applications (PMA'09). IEEE Computer Society, Beijing, China. 293-300.

Yan HP, Kang MZ, de Reffye P, Dingkuhn M. 2004. A Dynamic, Architectural Plant Model Simulating Resource-dependent Growth. Annals of Botany, 93: 591-602.

Wang F, Kang MZ, Lu Q, Han H, Letort V, Guo Y, de Reffye P, Li BG. 2009. Calibration of topological development in the procedure of parametric identification: application of the stochastic GreenLab model for Pinus sylvestris var. mongolica. In: Guo Y, Jaeger M eds. Proceedings of Plant Growth Modeling and Applications (PMA'09). IEEE Computer Society, Beijing, China. 26-33.